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Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

18. (Currently amended): A method for obtaining a profile of protein binding to the ~~genomic DNA~~ to genomic DNA of a biological sample comprising:
- a. obtaining a plurality of candidate fragments from the genomic DNA bound by a plurality of proteins, wherein the plurality of proteins comprise at least 50 proteins; by
eliminating unbound genomic DNA; and
 - b. detecting the candidate fragments.
19. (Original): The method of claim 18, wherein the candidate fragments are obtained by DNA foot printing.
20. (Currently amended): The method of Claim 19 wherein the step of ~~determining~~ detecting candidate fragments comprises hybridizing the candidate fragments with a collection of nucleic acid probes.
21. (Original): The method of Claim 20 wherein the nucleic acid probes are immobilized on a collection of beads or optical fibers.
22. (Original): The method of Claim 20 wherein the nucleic acid probes are immobilized on a substrate.
23. (Original): The method of Claim 22 wherein the collection of nucleic acid probes contains at least 10,000 probes.
24. (Original): The method of Claim 23 wherein the collection of nucleic acid probes

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contains at least 50,000 probes.

25. (Original): The method of Claim 24 wherein the collection of nucleic acid probes contains at least 100,000 probes.

26. (Original): The method of Claim 25 wherein the collection of nucleic acid probes contains at least 1,000,000 probes.

27. (Original): The method of Claim 26 wherein the nucleic acid probes are oligonucleotide probes.

28. (Currently amended): The method of Claim 27 wherein the oligonucleotide probes are between 10-50 nucleotides in length.

29. (Original): The method of Claim 28 wherein the oligonucleotide probes tile genomic sequences of interest.

30. (Original): The method of Claim 29 wherein the genomic sequences of interest contain genic regions.

31. (Currently amended): The method of claim 29, where ~~the~~ forward and lower strand sequences are tiled.

32. (Original): The method of Claim 31 wherein at least one of the binding proteins is unknown.